

0076964-000019SEQUENCE LISTING  
SEQUENCE LISTING

<110> Genomine, Inc.  
POSTECH FOUNDATION  
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<151> 2004-02-27  
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0076964-000019SEQLIST-revised.txt

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0076964-000019SEQLIST-revised.txt

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 210 215 220  
 Val Cys Gly Asp Val His Gly Gln Phe Tyr Asp Leu Leu Asn Ile Phe  
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 385 390 395 400  
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 405 410 415  
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 420 425 430  
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0076964-000019SEQLIST-revised.txt

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Thr Arg Gln Ile Leu Leu Ala Leu Pro Ser Leu Val Asp Ile Ser Val		
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0076964-000019SEQLIST-revised.txt

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 165 170 175  
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 Gly Val Lys Leu Ser Asp Ile Arg Ala Ile Asp Arg Phe Cys Glu Pro  
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cacatgaagt	
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Tyr Trp Ala Asn Arg Ala Phe Ala His Thr Lys Leu Glu Glu Tyr Gly  
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 Asp Phe Val Asp Arg Gly Ser Phe Ser Val Glu Ile Ile Leu Thr Leu  
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 His Phe His Leu Leu Arg Gly Asn His Glu Thr Asp Asn Met Asn Gln  
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Lys Gly Tyr Tyr Arg Arg Ala Ala Ser Asn Met Ala Leu Gly Lys Phe  
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0076964-000019SEQLIST-revised.txt

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Lys Ile Glu Arg Asn Arg Gln Pro Pro Asp Ser Gly Pro Met Cys Asp  
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450 455 460  
Leu Gln Gly Ser Asp Leu Arg Pro Gln Phe His Gln Phe Thr Ala Val  
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 Lys Phe Tyr Ser Gln Ala Ile Glu Leu Asn Pro Ser Asn Ala Ile Tyr  
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 Tyr Gly Asn Arg Ser Leu Ala Tyr Leu Arg Thr Glu Cys Tyr Gly Tyr  
 65 70 75 80  
 Ala Leu Gly Asp Ala Thr Arg Ala Ile Glu Leu Asp Lys Lys Tyr Ile  
 85 90 95  
 Lys Gly Tyr Tyr Arg Arg Ala Ala Ser Asn Met Ala Leu Gly Lys Phe  
 100 105 110  
 Arg Ala Ala Leu Arg Asp Tyr Glu Thr Val Val Lys Pro Asn Asp Lys  
 115 120 125  
 Asp Ala Lys Met Lys Tyr Gln Glu Cys Ser Lys Thr Val Lys Gln Lys  
 130 135 140  
 Gln Phe Glu Arg Ala Ile Ala Gly Asp Glu His Arg Arg Ser Val Val  
 145 150 155 160  
 Asp Ser Leu Asp Ile Glu Ser Met Thr Leu Glu Asp Glu Tyr Ser Gly  
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 Pro Lys Leu Glu Asp Gly Lys Val Thr Ile Thr Phe Met Lys Asp Leu  
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 Met Gln Trp Tyr Lys Asp Gln Lys Lys Leu His Arg Lys Cys Ala Tyr  
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 Gln Ile Leu Val Gln Val Lys Glu Val Leu Val Lys Leu Ser Thr Leu  
 210 215 220  
 Val Glu Thr Thr Leu Lys Glu Thr Glu Lys Ile Thr Val Cys Gly Asp  
 225 230 235 240  
 Thr His Gly Gln Phe Tyr Asp Leu Leu Asn Glu Phe Glu Leu Asn Gly  
 245 250 255  
 Leu Pro Ser Glu Thr Asn Pro Tyr Ile Glu Asn Gly Asp Phe Val Asp  
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 Arg Gly Ser Phe Ser Val Glu Val Ile Leu Thr Leu Phe Gly Phe Lys  
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Asp Asn Met Asn Gln Ile Tyr Gly Phe Glu Gly Glu Val Lys Ala Lys  
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Tyr Thr Ala Gln Met Tyr Glu Leu Phe Ser Glu Val Glu Glu Trp Leu  
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Pro Leu Ala Gln Cys Ile Asn Gly Lys Val Leu Ile Met His Gly Gly  
340 345 350

Leu Phe Ser Glu Asp Gly Val Thr Leu Asp Asp Ile Pro Lys Ile Glu  
355 360 365

Arg Asn Arg Gln Pro Phe Asp Ser Gly Pro Met Cys Asp Leu Leu Trp  
370 375 380

Ser Asp Pro Gln Pro Gln Asn Gly Arg Ser Val Ser Lys Arg Gly Val  
385 390 395 400

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405 410 415

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Glu Val Ala His Gly Gly Arg Cys Val Thr Val Phe Ser Ala Pro Asn  
435 440 445

Tyr Cys Asp Gln Met Gly Asn Lys Ala Ser Tyr Ile His Leu Gln Gly  
450 455 460

Ser Asp Leu Arg Pro Gln Phe His Gln Phe Thr Ala Val Pro His Pro  
465 470 475 480

Asn Val Lys Pro Met Ala Tyr Ala Asn Ile Leu Leu Gln Leu Gly Met  
485 490 495

Met

<210> 20  
<211> 513  
<212> PRT  
<213> *Saccharomyces cerevisiae*

<220>  
<221> PEPTIDE  
<222> (1)  
<223> PP5

<400> 20  
Met Ser Thr Pro Thr Ala Ala Asp Arg Ala Lys Ala Leu Glu Arg Lys  
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Asn Glu Gly Asn Val Phe Val Lys Glu Lys His Phe Leu Lys Ala Ile  
20 25 30

Glu Lys Tyr Thr Glu Ala Ile Asp Leu Asp Ser Thr Gln Ser Ile Tyr  
35 40 45

Phe Ser Asn Arg Ala Phe Ala His Phe Lys Val Asp Asn Phe Gln Ser  
50 55 60

## 0076964-000019SEQLIST-revised.txt

Ala Leu Asn Asp Cys Asp Glu Ala Ile Lys Leu Asp Pro Lys Asn Ile  
 65 70 75 80

Lys Ala Tyr His Arg Arg Ala Leu Ser Cys Met Ala Leu Leu Glu Glu  
 85 90 95

Lys Lys Ala Arg Lys Asp Leu Asn Val Leu Leu Lys Ala Lys Pro Asn  
 100 105 110

Asp Pro Ala Ala Thr Lys Ala Leu Leu Thr Cys Asp Arg Phe Ile Arg  
 115 120 125

Glu Glu Arg Phe Arg Lys Ala Ile Gly Gly Ala Glu Asn Glu Ala Lys  
 130 135 140

Ile Ser Leu Cys Gln Thr Leu Asn Leu Ser Ser Phe Asp Ala Asn Ala  
 145 150 155 160

Asp Leu Ala Asn Tyr Glu Gly Pro Lys Leu Glu Phe Glu Gln Leu Tyr  
 165 170 175

Asp Asp Lys Asn Ala Phe Lys Gly Ala Lys Ile Lys Asn Met Ser Gln  
 180 185 190

Glu Phe Ile Ser Lys Met Val Asn Asp Leu Phe Leu Lys Gly Lys Tyr  
 195 200 205

Leu Pro Lys Lys Tyr Val Ala Ala Ile Thr Ser His Ala Asp Thr Leu  
 210 215 220

Phe Arg Gln Glu Pro Ser Met Val Glu Leu Glu Asn Asn Ser Thr Pro  
 225 230 235 240

Asp Val Lys Ile Ser Val Cys Gly Asp Thr His Gly Gln Phe Tyr Asp  
 245 250 255

Val Leu Asn Leu Phe Arg Lys Phe Gly Lys Val Gly Pro Lys His Thr  
 260 265 270

Tyr Leu Phe Asn Gly Asp Phe Val Asp Arg Gly Ser Trp Ser Cys Glu  
 275 280 285

Val Ala Leu Leu Phe Tyr Cys Leu Lys Ile Leu His Pro Asn Asn Phe  
 290 295 300

Phe Leu Asn Arg Gly Asn His Glu Ser Asp Asn Met Asn Lys Ile Tyr  
 305 310 315 320

Gly Phe Glu Asp Glu Cys Lys Tyr Lys Tyr Ser Gln Arg Thr Phe Asn  
 325 330 335

Met Phe Ala Gln Ser Phe Glu Ser Leu Pro Leu Ala Thr Leu Ile Asn  
 340 345 350

Asn Asp Tyr Leu Val Met His Gly Gly Leu Pro Ser Asp Pro Ser Ala  
 355 360 365

Thr Leu Ser Asp Phe Lys Asn Ile Asp Arg Phe Ala Gln Pro Pro Arg  
 370 375 380

Asp Gly Ala Phe Met Glu Leu Leu Trp Ala Asp Pro Gln Glu Ala Asn  
 385 390 395 400

Gly Met Gly Pro Ser Gln Arg Gly Leu Gly His Ala Phe Gly Pro Asp  
 405 410 415

Ile Thr Asp Arg Phe Leu Arg Asn Asn Lys Leu Arg Lys Ile Phe Arg  
 420 425 430

0076964-000019SEQLIST-revised.txt

Ser His Glu Leu Arg Met Gly Gly Val Gln Phe Glu Gln Lys Gly Lys  
435 440 445  
Leu Met Thr Val Phe Ser Ala Pro Asn Tyr Cys Asp Ser Gln Gly Asn  
450 455 460  
Leu Gly Gly Val Ile His Val Val Pro Gly His Gly Ile Leu Gln Ala  
465 470 475 480  
Gly Arg Asn Asp Asp Gln Asn Leu Ile Ile Glu Thr Phe Glu Ala Val  
485 490 495  
Glu His Pro Asp Ile Lys Pro Met Ala Tyr Ser Asn Gly Gly Phe Gly  
500 505 510  
Leu

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<211> 520  
<212> PRT  
<213> Drosophila melanogaster

<220>  
<221> PEPTIDE  
<222> (1)  
<223> PP5

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Glu Glu Asp Thr Asn Ala Arg Thr Lys Ala Glu Leu Asp Phe Ala Ala  
35 40 45  
Ala Glu Gln Tyr Lys Asn Gln Gly Asn Glu Met Leu Lys Thr Lys Glu  
50 55 60  
Phe Ser Lys Ala Ile Asp Met Tyr Thr Lys Ala Leu Glu Leu His Pro  
65 70 75 80  
Asn Ser Ala Ile Tyr Tyr Ala Asn Arg Ser Leu Ala His Leu Arg Gln  
85 90 95  
Glu Ser Phe Gly Phe Ala Leu Gln Asp Gly Val Ser Ala Val Lys Ala  
100 105 110  
Asp Pro Ala Tyr Leu Lys Gly Tyr Tyr Arg Arg Ala Ala Ala His Met  
115 120 125  
Ser Leu Gly Lys Phe Lys Gln Ala Leu Cys Asp Phe Glu Phe Val Ala  
130 135 140  
Lys Cys Arg Pro Asn Asp Lys Asp Ala Lys Ile Lys Phe Thr Glu Cys  
145 150 155 160  
Asn Lys Thr Val Lys Met Arg Ala Phe Glu Arg Ala Ile Ala Val Asp  
165 170 175  
Lys Pro Glu Lys Thr Leu Ser Glu Met Tyr Ser Asp Met Glu Asn Ile  
180 185 190

Thr Ile Glu Asp Asp Tyr Lys Gly Pro Gln Leu Glu Asp Gly Lys Val  
 195 200 205  
 Thr Leu Lys Phe Met Lys Glu Leu Met Glu His Thr Lys Ala Gln Lys  
 210 215 220  
 Arg Leu His Arg Lys Phe Ala Tyr Lys Ile Leu Cys Glu Ile Asp Thr  
 225 230 235 240  
 Tyr Met Arg Ala Gln Pro Ser Leu Val Asp Ile Thr Val Pro Asp Glu  
 245 250 255  
 Glu Lys Glu Thr Ile Cys Gly Asp Ile His Gly Gln Phe Tyr Asp Leu  
 260 265 270  
 Met Asn Ile Phe Glu Ile Asn Gly Leu Pro Ser Glu Lys Asn Pro Tyr  
 275 280 285  
 Leu Phe Asn Gly Asp Phe Val Asp Arg Gly Ser Phe Ser Val Glu Cys  
 290 295 300  
 Ile Glu Thr Leu Phe Gly Phe Lys Leu Leu Tyr Pro Asn His Phe Phe  
 305 310 315 320  
 Leu Ala Arg Gly Asn His Glu Ser Ile Asn Met Asn Gln Met Tyr Gly  
 325 330 335  
 Glu Thr Gly Glu Val Thr Ala Lys Tyr Thr Ser Ala Met Ala Asp Ile  
 340 345 350  
 Phe Thr Gln Val Glu Asn Trp Leu Pro Leu Cys His Cys Ile Asn Gln  
 355 360 365  
 Lys Ile Leu Val Met His Gly Gly Leu Phe Ser Thr Glu Asp Val Thr  
 370 375 380  
 Leu Asp His Ile Arg Arg Ile Glu Arg Asn Cys Gln Pro Pro Glu Glu  
 385 390 395 400  
 Gly Leu Met Cys Glu Leu Leu Trp Ser Asp Pro Gln Gln Trp Met Gly  
 405 410 415  
 Leu Gly Gln Ser Lys Arg Gly Val Gly Ile Gln Phe Gly Pro Asp Val  
 420 425 430  
 Thr Glu Lys Glu Cys Lys Asp Asn Asn Leu Asp Tyr Ile Ile Arg Ser  
 435 440 445  
 His Glu Val Lys Asp Met Gly Tyr Glu Val Ala His Asn Gly Lys Cys  
 450 455 460  
 Ile Thr Val Phe Ser Ala Pro Asn Tyr Cys Asp Thr Met Gly Asn Met  
 465 470 475 480  
 Gly Ala Phe Ile Thr Ile Thr Gly Asn Asn Leu Lys Pro Asn Tyr Lys  
 485 490 495  
 Ser Phe Glu Ala Val Pro His Pro Asp Val Lys Pro Met Ala Tyr Ala  
 500 505 510  
 Asn Ser Leu Met Asn Trp Leu Ala  
 515 520

<210> 22  
 <211> 524  
 <212> PRT

<213> *Caenorhabditis elegans*

<220>  
<221> PEPTIDE  
<222> (1)  
<223> PP5

<400> 22  
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Ile Glu Glu Lys Ser Tyr Glu Asp Glu Lys Glu Lys Ala Gly Met Ile  
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Lys Asp Glu Ala Asn Gln Phe Phe Lys Asp Gln Val Tyr Asp Val Ala  
35 40 45  
Ala Asp Leu Tyr Ser Val Ala Ile Glu Ile His Pro Thr Ala Val Leu  
50 55 60  
Tyr Gly Asn Arg Ala Gln Ala Tyr Leu Lys Lys Glu Leu Tyr Gly Ser  
65 70 75 80  
Ala Leu Asp Asp Ala Asp Asn Ala Ile Ala Ile Asp Pro Ser Tyr Val  
85 90 95  
Lys Gly Phe Tyr Arg Arg Ala Thr Ala Asn Met Ala Leu Gly Arg Phe  
100 105 110  
Lys Lys Ala Leu Thr Asp Tyr Gln Ala Val Val Lys Val Cys Pro Asn  
115 120 125  
Asp Lys Asp Ala Arg Ala Lys Phe Asp Glu Cys Ser Lys Ile Val Arg  
130 135 140  
Arg Gln Lys Phe Glu Ala Ala Ile Ser Thr Asp His Asp Lys Lys Thr  
145 150 155 160  
Val Ala Glu Thr Leu Asp Ile Asn Met Ala Ile Glu Asp Ser Tyr Asp  
165 170 175  
Gly Pro Arg Leu Glu Asp Lys Ile Thr Lys Glu Phe Val Leu Gln Leu  
180 185 190  
Ile Lys Thr Phe Lys Asn Gln Gln Lys Leu His Lys Lys Tyr Ala Phe  
195 200 205  
Lys Met Leu Leu Glu Phe Tyr Asn Tyr Val Lys Ser Leu Pro Thr Met  
210 215 220  
Val Glu Ile Thr Val Pro Thr Gly Lys Lys Phe Thr Ile Cys Gly Asp  
225 230 235 240  
Val His Gly Gln Phe Tyr Asp Leu Cys Asn Ile Phe Glu Ile Asn Gly  
245 250 255  
Tyr Pro Ser Glu Thr Asn Pro Tyr Leu Phe Asn Gly Asp Phe Val Asp  
260 265 270  
Arg Gly Ser Phe Ser Val Glu Thr Ile Phe Thr Met Ile Gly Phe Lys  
275 280 285  
Leu Leu Pro Asn His Phe Phe Met Ser Arg Gly Asn His Glu Ser Asp  
290 295 300  
Val Met Asn Lys Met Tyr Gly Phe Glu Gly Glu Val Lys Ala Lys Tyr  
305 310 315 320

0076964-000019SEQLIST-revised.txt

Thr Gln Gln Met Cys Asp Met Phe Thr Glu Thr Phe Cys Trp Leu Pro  
325 330 335

Leu Cys His Leu Ile Asn Glu Lys Ile Phe Val Cys His Gly Gly Leu  
340 345 350

Phe Lys Glu Asp Gly Val Thr Leu Glu Asp Ile Arg Lys Thr Asp Arg  
355 360 365

Asn Arg Gln Pro Pro Asp Glu Gly Ile Met Cys Asp Leu Leu Trp Glu  
370 375 380

Lys Asn Trp Lys Asn Leu Lys Ile Leu Tyr Pro Asp Gly Lys Ile Asn  
385 390 395 400

Lys Asn Ser Asn Cys Gln Pro Lys Thr Cys Lys Asn Ala Ser Asp Pro  
405 410 415

Gln Pro Ile Asn Gly Arg Ser Pro Ser Lys Arg Gly Val Gly Cys Gln  
420 425 430

Phe Gly Pro Asp Val Thr Ser Lys Trp Cys Glu Thr Asn Gly Ile Glu  
435 440 445

Tyr Val Val Arg Ser His Glu Val Lys Pro Glu Gly Tyr Glu Met His  
450 455 460

His Asn Gly Gln Cys Phe Thr Val Phe Ser Ala Pro Asn Tyr Cys Asp  
465 470 475 480

Gln Met Asn Asn Lys Gly Ala Phe Ile Thr Ile Thr Gly Asp Asn Leu  
485 490 495

Thr Pro Arg Phe Thr Pro Phe Asp Ala Val Pro His Pro Lys Leu Pro  
500 505 510

Pro Met Ala Tyr Ala Asn Ser Leu Phe Gly Phe Asn  
515 520

<210> 23  
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<212> PRT  
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<220>  
<223> PP2A motif

<220>  
<221> misc\_feature  
<222> (3)..(3)  
<223> Xaa can be any naturally occurring amino acid

<400> 23  
Gly Asp Xaa His Gly Gln  
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<210> 24  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
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<220>  
<221> misc\_feature

0076964-000019SEQLIST-revised.txt

<222> (3)..(3)  
<223> Xaa can be any naturally occurring amino acid

<220>  
<221> misc\_feature  
<222> (5)..(5)  
<223> Xaa can be any naturally occurring amino acid

<400> 24  
Gly Asp xaa val xaa Arg Gly  
1 5

<210> 25  
<211> 5  
<212> PRT  
<213> Artificial sequence

<220>  
<223> PP2A motif

<400> 25  
Arg Gly Asn His Glu  
1 5

<210> 26  
<211> 6  
<212> PRT  
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<220>  
<223> C-terminal consensus sequence

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Ser Ala Pro Asn Tyr Cys  
1 5